

Sign test

(H₀: data are iid)

- One sample (Z sided): X_1, \dots, X_n

$$\begin{cases} H_0: P(X > c_0) = q \\ H_1: P(X > c_0) \neq q \end{cases}$$

(if $q = 0.5$:

$$\begin{cases} H_0: \text{MED}(X) = c_0 \\ H_1: \text{MED}(X) \neq c_0 \end{cases}$$

if the distribution is symmetric this is also a test for the mean (if \exists)

Test statistic: $W = \sum_{i=1}^n \mathbb{1}_{\{X_i > c_0\}} \in \{0, \dots, n\}$

Under H_0 : $W \sim \text{Bi}(n, q)$

Under H_1 : $W \sim \text{Bi}(n, p)$ $p \neq q$

$$\Rightarrow \begin{cases} H_0: W \sim \text{Bi}(n, q) \\ H_1: W \sim \text{Bi}(n, p), p \neq q \end{cases}$$

this is the test that we perform

Test statistic (another formulation): $W = \frac{n + \sum_{i=1}^n \text{sign}(X_i - c_0)}{2}$

- Two samples - paired $\rightarrow (X_1, Y_1), \dots, (X_n, Y_n) \rightarrow Z_1, \dots, Z_n \rightarrow$ one sample

$$\begin{cases} H_0: P(X > Y) = q \\ H_1: P(X > Y) \neq q \end{cases} = \begin{cases} H_0: P(Z > 0) = q \\ H_1: P(Z > 0) \neq q \end{cases}$$

we're testing the H₀ that in a random pair (X,Y), X has the same probability of being larger or smaller than Y

Rank test: Mann-Whitney U-test

(H₀: X_i iid, Y_i iid, $\{X_i\} \perp \{Y_i\}$)

- Two samples: $X_1, \dots, X_n \stackrel{\text{iid}}{\sim} X, Y_1, \dots, Y_m \stackrel{\text{iid}}{\sim} Y$

$$\begin{cases} H_0: P(X > Y) = \frac{1}{2} \\ H_1: P(X > Y) \neq \frac{1}{2} \end{cases}$$

Test statistics: $U_1 = \sum_{i=1}^n \sum_{j=1}^m \mathbb{1}_{\{X_i > Y_j\}} = n \cdot m \cdot \hat{P}(X > Y)$, $U_2 = \sum_{i=1}^n \sum_{j=1}^m \mathbb{1}_{\{Y_j > X_i\}} = n \cdot m \cdot \hat{P}(Y > X)$

under H_0 they have the same distribution

Computationally:

- $X = (X_1, \dots, X_n, Y_1, \dots, Y_m)$, $\dim(X) = n+m$

- $R = (r(X_1), \dots, r(X_n), r(Y_1), \dots, r(Y_m))$

$$r(X_i) = \sum_{\text{elem} \in X} \mathbb{1}_{\{X_i \geq \text{elem}\}} = \# \text{ wins/ties of } X_i \text{ vs. } X$$

$$r(Y_j) = \sum_{\text{elem} \in X} \mathbb{1}_{\{Y_j \geq \text{elem}\}} = \# \text{ wins/ties of } Y_j \text{ vs. } X$$

if $r(\text{element}) = 1$ (the element's rank is 1) then the element is the worst player (we look at it as a contest of team X vs. team Y)

- $R_1 = \sum_{i=1}^n r(X_i) = \sum \text{ranks of } X$

$$R_2 = \sum_{j=1}^m r(Y_j) = \sum \text{ranks of } Y$$

- $U_1 = R_1 - \frac{n(n+1)}{2}$, $U_2 = R_2 - \frac{m(m+1)}{2}$

\downarrow #ties/wins of the first sample (X) against the pooled sample (X)
 \rightarrow #wins/ties of the first sample against itself

Signed-Rank test: Wilcoxon

(H₀: data are iid)

- One sample: X_1, \dots, X_n

$$\begin{cases} H_0: P(X > c_0) = q \\ H_1: P(X > c_0) \neq q \end{cases}$$

Test statistic: $W^+ = \sum_{i=1}^n \mathbb{1}_{\{X_i > c_0\}} R(|X_i - c_0|)$

Under H_0 : $[\mathbb{1}_{\{X_i > c_0\}} \sim \text{Be}(q)] \perp [R(|X_i - c_0|) \sim \mathcal{U}(\{1, 2, \dots, n\})]$

under H_1 $\mathbb{1}_{\{X_i > c_0\}} \sim \text{Be}(p)$ with $p \neq q$ and $\mathbb{1}_{\{X_i > c_0\}}$ and $R(|X_i - c_0|)$ are not \perp

- Two samples - paired $\rightarrow (X_1, Y_1), \dots, (X_n, Y_n) \rightarrow Z_i = X_i - Y_i$

$$\begin{cases} H_0: P(X > Y) = q \\ H_1: P(X > Y) \neq q \end{cases} = \begin{cases} H_0: P(Z > 0) = q \\ H_1: P(Z > 0) \neq q \end{cases}$$

Test statistic (\uparrow): $W^+ = \sum_{i=1}^n \mathbb{1}_{\{X_i > Y_i\}} R(|X_i - Y_i|)$

Permutation test: 2 samples

(Hp. X_{1i} iid, X_{2i} iid, $\{X_{1i}\} \perp \{X_{2i}\}$)

$$\begin{aligned} X_{11}, X_{12}, \dots, X_{1n_1} &\stackrel{\text{iid}}{\sim} X_1 \\ X_{21}, X_{22}, \dots, X_{2n_2} &\stackrel{\text{iid}}{\sim} X_2 \end{aligned}$$

$$\begin{cases} H_0: X_1 \stackrel{d}{=} X_2 \\ H_1: X_1 \stackrel{d}{\neq} X_2 \end{cases}$$

Test statistic: $T_0 = |\bar{X}_1 - \bar{X}_2| \rightarrow$

- Compute T_0 of the original sample
- $X_{\text{pooled}} = (X_{11}, \dots, X_{1n_1}, X_{21}, \dots, X_{2n_2})$

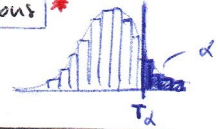
$\pi(X_{\text{pooled}})$ = permutation of X_{pooled}

- Compute $T = T(\pi(X_{\text{pooled}}))$ permutation π

- p-value = $\# \{T \geq T_0\} / \# \text{permutations}$ *

- critical region = $\{T_0 : T_0 \geq T_{\alpha}\}$

T_{α} = superior α quantile



* if considering all the perm.s is too expensive \Rightarrow we consider only **B random permutations**

Permutation test: One-Way ANOVA

(Hp. X_{ji} iid \sim group j , \perp among groups)

$$X_{j1}, \dots, X_{jn_j} \stackrel{\text{iid}}{\sim} X_j \quad j = 1, \dots, G$$

$$\begin{cases} H_0: X_1 \stackrel{d}{=} X_2 \stackrel{d}{=} \dots \stackrel{d}{=} X_G \\ H_1: \exists i, j \text{ s.t. } X_i \stackrel{d}{\neq} X_j \end{cases}$$

Test statistic (from the param. case):
(There are other choices, this one is sensitive w.r.t. shifts)

$$T_0 = \frac{\sum_{j=1}^G n_j (\bar{x}_j - \bar{x})^2}{\sum_{j=1}^G \sum_{i=1}^{n_j} (x_{ji} - \bar{x}_j)^2}$$

Permutation test: simple regression

- (Hp. 1. The conditional mean of Y increases/decreases linearly in the value of X
2. The error is an additive error
3. The errors are iid)

$$Y_i | X_i = x_i = \beta_0 + \beta_1 x_i + \varepsilon_i \quad \varepsilon_i \stackrel{\text{iid}}{\sim} \varepsilon$$

$$\begin{cases} H_0: \beta_1 = 0 \\ H_1: \beta_1 \neq 0 \end{cases} = \begin{cases} H_0: Y_1, \dots, Y_n \stackrel{\text{iid}}{\sim} Y = \beta_0 + \varepsilon \\ H_1: Y_1, \dots, Y_n \not\sim \text{iid} : Y_i = \beta_0 + \beta_1 x_i + \varepsilon_i \end{cases}$$

Test statistic: $T_0 = \left(\frac{\sum_{i=1}^n (x_i - \bar{x}_n)(y_i - \bar{y}_n)}{\sum_{i=1}^n (x_i - \bar{x}_n)^2} \right)^2$

Idea: under H_0 the new combination of \vec{Y} -responses will have the same probability of being observed as the original. This is not true under H_1 .

Permutation test: center of symmetry

(Hp. data are iid)

$$X_1, \dots, X_n \stackrel{\text{iid}}{\sim} X \text{ s.t. } \exists c: f(c+h) = f(c-h) \quad \forall h \in \mathbb{R}$$

$$\begin{cases} H_0: c = c_0 \\ H_1: c \neq c_0 \end{cases}$$

Test statistic: $T_0 = |\bar{X}_n - c_0|$

Transformations: $\pi(X_1, \dots, X_n)$ = every element can be taken as it is or flipped on the other side of the symmetry (\neq permutation)

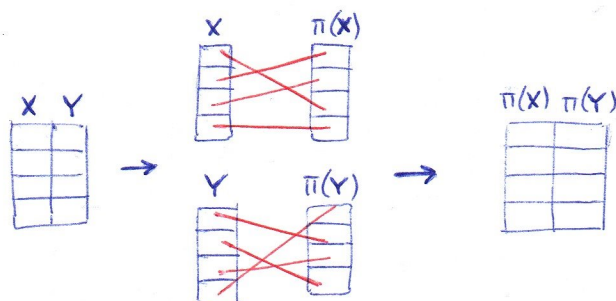
Idea: under H_0 , since we have symmetry, a datum taken on one side of the symmetry or the other (with the same distance w.r.t. the symmetry) has the same impact on the likelihood

Permutation test: independence

$$(X_1, Y_1), \dots, (X_n, Y_n) \stackrel{\text{iid}}{\sim} (X, Y)$$

$$\begin{cases} H_0: X \perp Y \\ H_1: X \not\perp Y \end{cases}$$

Idea: under H_0 the new sample $(\pi(X), \pi(Y))$ will have the same probability of being obtained than the original one.



Permutation test: 2 || samples multivariate

(Hp. X_{1i} iid, X_{2i} iid, $\{X_{1i}\}_i \perp \{X_{2i}\}_i$)

$$X_{11}, X_{12}, \dots, X_{1n_1} \stackrel{\text{iid}}{\sim} X_1$$

$$X_{21}, X_{22}, \dots, X_{2n_2} \stackrel{\text{iid}}{\sim} X_2$$

$$H_0: X_1 \stackrel{d}{=} X_2$$

$$H_1: X_1 \not\stackrel{d}{=} X_2$$

$$\text{Test statistic: } \|\bar{X}_1 - \bar{X}_2\|_{\mathbb{R}^p}^2 = T_0$$

Permutation test: center of symmetry multivariate

(Hp. data are iid)

$$X_1, \dots, X_n \stackrel{\text{iid}}{\sim} X \in \mathbb{R}^p \text{ s.t. } \exists c \in \mathbb{R}^p: f(c+h) = f(c-h) \quad \forall h \in \mathbb{R}^p$$

$$H_0: c = c_0$$

$$H_1: c \neq c_0$$

$$\text{Test statistic: } T_0 = \|\bar{X}_n - c_0\|_{\mathbb{R}^p}^2$$

Transformations: $\pi(X_1, \dots, X_n)$ = each element is taken as it is or flipped (the whole vector is flipped)

Permutation test: regression-multiple

(Hp. linearity of the conditional mean w.r.t. the regressors,

$$Y_i | X_{1i} = x_{1i}, X_{2i} = x_{2i} = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + \varepsilon_i \quad \varepsilon_i \stackrel{\text{iid}}{\sim} \varepsilon$$

additive action on the response of the error term, errors iid)

Global test: (F-test)

$$H_0: (\beta_1, \beta_2) = (0, 0)$$

$$H_1: (\beta_1, \beta_2) \neq (0, 0)$$

$$= \begin{cases} H_0: Y_1, \dots, Y_n \stackrel{\text{iid}}{\sim} Y = \beta_0 + \varepsilon \\ H_1: Y_1, \dots, Y_n \not\stackrel{\text{iid}}{\sim} Y = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \varepsilon \end{cases}$$

Transformations: permutations of residuals *

Test statistic: F-statistic (it considers also the covariances)

Partial test: (t-test)

$$H_0: \beta_1 = 0$$

$$H_1: \beta_1 \neq 0$$

$$= \begin{cases} H_0: Y_i - (\beta_0 + \beta_2 X_{2i}) = \varepsilon_i \stackrel{\text{iid}}{\sim} \varepsilon \\ H_1: Y_i - (\beta_0 + \beta_2 X_{2i}) = \beta_1 X_{1i} + \varepsilon_i \not\stackrel{\text{iid}}{\sim} \varepsilon \end{cases}$$

Transformations: permutations of residuals *

Test statistic: t-test

* Procedure:
(Freedman and Lane)

- Evaluate T_0 (test statistic (t/F) on the complete model
- calculate the residuals on the reduced model (H_0)

- permute the residuals
- new data = fitted values of the original (complete) model + permuted residuals

- Test statistic on the complete model with new data

- p-value = $\#(\text{test.stat.perm} \geq \text{test.stat.original}) / \# \text{iterations (loop)}$

on loop

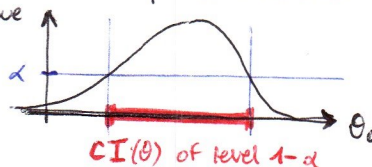
→ The null model enters for estimating the residuals

→ The complete model enters for the test statistic

Permutational Confidence Intervals

$$CI(\theta)? \rightarrow \begin{cases} H_0: \theta = \theta_0 \\ H_1: \theta \neq \theta_0 \end{cases}$$

- Find the right test from the above,
- select a grid of values for θ_0 ,
- perform the test chosen with all the values of θ_0 in the grid finding the p-values (one p-value for each θ_0),
- consider the p-value function:



$$CI_{1-\alpha}(\theta) = \{\theta_0: p\text{-value}(\theta_0) \geq \alpha\}$$

This means to go to the first reachable level α from below (it's a discrete function the p-val's)

Bootstrap

$X_1, \dots, X_n : X_0 = [X_1 | X_2 | \dots | X_n] \rightarrow X_1, X_2, \dots, X_B : [X_i]_j = \text{sampled from } X_0$
 (each element has $1/n$ prob. to be sampled)
 $X_1, \dots, X_B \rightarrow \hat{\theta}_1^*, \dots, \hat{\theta}_B^* \rightarrow$ we can build the cumulative distribution
 parameter of interest

Confidence Intervals: (Reverie-Percentile CI) \rightarrow bootstrapping of $\hat{\theta} - \theta$

Once we have the distribution of the estimator (bootstrap distribution), we compute the superior quantile $\alpha/2$ and the inferior quantile $1 - \alpha/2$:

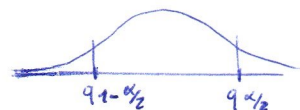
$$CI_{1-\alpha}(\theta) : 2\hat{\theta} - \hat{\theta}_{\alpha/2}^* < \theta < 2\hat{\theta} - \hat{\theta}_{1-\alpha/2}^*$$

Notations:

only asymptotically exact
 (if n is small \Rightarrow they have a real coverage which is smaller than the nominal)

$\hat{\theta}$ = parameter of interest's estimate with X_0

$\hat{\theta}_{\alpha/2}^*, \hat{\theta}_{1-\alpha/2}^*$ = quantiles of the bootstrap distribution



Confidence Intervals: (T intervals) \rightarrow bootstrapping of $\frac{\hat{\theta} - \theta}{\hat{\sigma}_{\hat{\theta}}}$

$$CI_{1-\alpha}(\theta) : \hat{\theta} - t_{\alpha/2}^* \hat{\sigma}_{\hat{\theta}} < \theta < \hat{\theta} - t_{1-\alpha/2}^* \hat{\sigma}_{\hat{\theta}}$$

estimate associated to the original sample (X_0)

quantiles of the bootstrap distribution of:

$$\frac{\hat{\theta}^* - \hat{\theta}}{\hat{\sigma}_{\hat{\theta}}^*}$$

* estimate of the standard deviation of the estimator computed on the bootstrap sample

Procedure:

- Evaluate $\hat{\theta}$ on X_0

- Create X_i : sampling from X_0 (with rep.)
- Evaluate $\hat{\theta}^*$ on X_i (same formula; diff. sample)
- Evaluate $(\hat{\theta}^* - \hat{\theta}) / \hat{\sigma}_{\hat{\theta}}^* = T^*$

- Given the T^* for every bootstrapped sample, find the quantiles $\alpha/2$ and $1 - \alpha/2$ on loop (B)
- $CI_{1-\alpha}(\theta) : (\uparrow)$ where $\hat{\sigma}_{\hat{\theta}} \neq \hat{\sigma}_{\hat{\theta}}^*$
 (In CI we use the one from the original sample)

We need $\hat{\sigma}_{\hat{\theta}} / \hat{\sigma}_{\hat{\theta}}^*$:
 in the case of proportion (date which are prob.) the standard dev. is given by:

$$\sqrt{\frac{p(1-p)}{n}}$$

- Approaches:
 - NAIVE (\uparrow): resampling from the same sample
 - SMOOTH: we smooth the empirical distribution
 - PARAMETRIC: we know the family but not the parameters

Regression: (CI for regression)

$$Y_i | X_i = x_i = \beta_0 + \beta_1 x_i + \epsilon_i, \quad \epsilon_i \stackrel{iid}{\sim} \epsilon$$

Procedure:

- Fit the regression model under H_1 * and obtain T_0 .
- compute the residuals (values - fitted values) \leftarrow residuals from the H_1 model
- new data = fitted values from * + sampled residuals (from residuals)
- Fit with new data (H_1) and obtain T
- Given T for every bootstrap case \rightarrow bootstrap distr. and CI (\uparrow)

Z/more \perp samples

we independently bootstrap the different samples.

Test & p-values

$$\begin{cases} H_0: \theta = \theta_0 \\ H_1: \theta \neq \theta_0 \end{cases} \rightarrow \text{Through the previous procedures we obtain } CI_{1-\alpha}(\theta)$$

Varying α we may contain or not θ_0 : the p-value of the test is the smallest α for which $CI_{1-\alpha}$ does not contain θ_0 .

(we do a grid for α that we want consider, we evaluate $CI_{1-\alpha}$ for every α and we check if θ_0 is inside. The smallest α for which θ_0 is not in the interval \rightarrow p-value)